Molecular Epidemiology of Extended-Spectrum β-lactamases among Klebsiella pneumoniae Isolates Collected in ICU Namazi Hospital, Shiraz

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Background & Objectives: The occurrence of Extended Spectrum β Lactamases (ESBL) producing *Klebsiella pneumoniae* has been seadity increased in recent ears, resulting in limitation of therapeutic options. In this study we used a multiplex PCR to identify three genes (TEM, SHV, CTX–M) in *Klebsiella pneumonia* isolates.

Methods: Sixty isolates of *K. pneumoniae* were received from different clinical specimens. Then primary drug resistant pattern of them to 10 antibiotics were determined and subsequently by means of double disk synergy test in respect to extended_spectrum β_lactamas were assessed and The MICs for cefotaxim were also determined using E. test stirp. Multiplex PCR for was used to identify CTX-M,SHV,TEM genes in *Klebsiella pneumoniae* isolates.

Results: The primary susceptibility tests *K. pneumoniae* showed that among 10 examined antibiotics, the most resistant was to ampicillin and the most susceptibility was to imipenem. The determination of ESBL phenotypically by DDST showed that 60% isolates produced ESBL. Multiplex PCR of the genes among *K. pneumoniae* isolates showed that 39% of them have TEM,%39 of them have both CTX-M and TEM and %13 of them have TEM,SHV,CTX-M.

Conclusion: Our finding showed that the high prevalence of ESBL producing *Klebsiella pneumonia* from ICU patients. Rational so adiministraion of β lactamas and appropriate infection control policies may reduce prevalence of ESBL producing bacteria in ICUs .

Keywords: *Klebsiella pneumoniae*; ESBL; MultiplexPCR; TEM; SHV; CTX–M